GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

August 9, 2003, 16:11:58; Search time 9.77143 Seconds (Without alignments) 91.441 Million cell updates/sec Run on:

US-09-905-691-2 19 1 ARARRAARAARRARAEA 19

Title: Perfect score: Sequence:

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

127863 segs, 47026705 residues Searched:

Word size :

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Q9rzs4 delnococcus	Н	bradyr	_	_	_	therm	O87840 streptomyce	_	ъ			_	_		Pl1092 bordetella	-	-			_	-	_	-	Q9a9e5 caulobacter	_	P03179 epstein-bar		-	_	_	Q06424 bacterlopha	_
SUMMARIES	ព	3	VCO7_ADE04	CCMC_BRAJA	YM32_MYCTU	YOB3_CAUCR	CKRA_HUMAN	ARGJ_THETH	SUC2_STRCO	ARGJ_METKA		PROA_MEIRU	CESS_HUMAN	Y486_MYCLE	VGLX_HSVBS	TRME_XANAC	CYAE_BORPE	Y486_MYCTU	GSHR_PLAF7	GSHR_PLAFK	EX71_RHILO	US26_HCMVA	HEM1_AGABI	UL47_HSVBP	METE_CAUCR	SYFB_CAUCR	VGLB_PRVIF	VP14_EBV	HAP_HAEIN	SPCP_HUMAIN	DY HB_HUMAN	RPOZ_NEIMA	- 1	RPOZ_HAEIN
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RPOZ_PASMU RPOZ_VIBCH RPOZ_VIBPA RPOZ_VIBPA RPOZ_ECCLI RPOZ_FERPE RPOZ_YERPE NIFW_RNCTU NIFW_RNCSH UL67_HCMYA RL18_HAEIN VGLJ_HSVSB
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132 AARRAAR 138 3 AARRAAR 9 ò g

RESULT 2 VCO7_ADE04 ID VCO7_ADE04

PRT; 193 AA. STANDARD;

us-09-905-691-2.olig.rsp

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-1 - FUNCTION: REQUIRED FOR THE EXPORT OF HEME TO THE PERIPLASM FOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              AP005936;
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RRANSMEM 19
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YM32_MYCTU
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Matches
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Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
15-SEP-2003 (Rel. 44), Last annotation update)
Heme exporter protein C (Cytochrome c-type biogenesis protein cyc2).
CYCZ OR CCMC OR BLR0469.
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                                                                                                                                                                Human adenovirus type 4.
Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
NCBL_TaxID=28280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bradyrhizobium japonicum USDA110.";
DNA Res. 9:189-197(2002).
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CLEAVAGE (BY ADENOVIRUS PROTEASE)
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Bradyrhizobiaceae; Bradyrhizobium.
                                                                                                                                                                                                                                                                                                                          STRAIN-Isolate RI-6;
Tarassishin L., Szawlowski P.W.S., McLay J., Russell W.C.,
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 193;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43137E07DB379DD0 CRC64;
                        01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Major core protein precursor (Protein VII) (pVII).
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100.0%; Pred. No....
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PF03228; Adeno_VII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              193 AA; 21358 MW;
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| 135 RAARRAA 141
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P30962;
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CCMC_BRAJA
AC P309621
DT P1-JUL.
DT 11-JUL.
DT 15-JUL.
DT 15-JUL.
DT 15-JUL.
DX CKDE CT.
CC BACTET.
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Cole S.T., Broach R., Parkhill J., Garnier T., Churcher C., Harris D. Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,

Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,

Davies R., Deviin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,

Hornsby T., Jagels R., Krogh A., McLean J., Woule S., Murphy L.,

Oliver S., Osborne J., Quall M.A., Rajandream M.A., Rogers J.,

Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;

"Deciphering the blology of Mycobacterium tuberculosis from the
                            -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Elsen J.A., Carpenter L., White O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 263;
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InterPro; IPR002541; Cytc_asm.
InterPro; IPR003557; Cytc_blog_ccmC.
Pfam; PF01578; Cytc_asm. 1.
PRINTS; PR01386; CCMCINGNSIS.
TIGREAMS; TIGR01191; ccmC; 1.
Cytochrome c-type blogenesis; Transport; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
A02EF75769F94EC0 CRC64;
                                                  (Probable).
-1- SIMILARITY: BELONGS TO THE CCMC/CYCZ/HELC FAMILY.
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01-00T-1996 (Rel. 34, Created)
16-00T-2001 (Rel. 40, Last sequence update)
28-FRS-2003 (Rel. 41, Last annotation update)
Hypothetical protein RV2232/RV2233.
RV2232/RV2233 OR MT2292 OR MTCY427.13/MTCX427.14.
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39 POTENTIAL
BIOGENESIS OF C-TYPE CYTOCHROMES
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                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M60874; AAA26194.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND CHARACTERIZATION.
MEDLIFE-20191997; PubMed-10725666;
Jarmin D.I., Rits M., Bota D., Gerard N.P., Graham G.J.,
Clark-Lewis I., Gerard C.,
"Identification of the orphan receptor G-protein-coupled receptor 2 as
CCR10, a specific receptor for the chemokine Eskine.";
JIRMUNDOI. 164:3460-3464(2000).
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MEDLINE-95154831; PubMed=7851889;
MAICHESE A., Docherty J.M., Nguyen T., Heiber M., Cheng R.,
Heng H.H.O., Tsul L.-C., Shi X., George S.R., O'Dowd B.F.;
"Cloning of human genes encoding novel G protein-coupled receptors.";
Genomics 23:609-618(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homey B., Wang W., Soto H., Buchanan M.E., Wiesenborn A., Catron D., Muller A., McClanahan T.K., Dieu-Nosjean M.C., Orozco R., Ruzicka T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lehmann P., Oldham E., Zlotnik A., "The orphan chemokine receptor-2 (GPR-2, CCR10) binds the skin-associated chemokine CCL27 (CTACK/ALP/ILC).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CKRA_HUMAN STANDARD; PRT; 362 AA.
D46092; 09NZ62;
D400-1995 (Rel. 32, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
C-C chemokine receptor type 10 (C-C CKR-10) (CC-CKR-10)
Protein coupled receptor 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    36.8%; Score 7; DB 1; Length 326; 100.0%; Pred. No. 19; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                            ATP (POTENTIAL).
N -> K (IN REF. 1).
1; 3F58765201CEF32D CRC64;
                                                                                                                                                                                                                                                                InterPro:
InterPro:
InterPro:
Pfam: PF0308; ArgK; 1.
SMART: SM00382; AAA; 1.
TIGR00780; Iao; 1.
Hypcthetical protein; ATP-binding; Complete proteome.
61 ATP (POTENTIAL).
77 N -> K (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND CHARACTERIZATION. MEDLINE-20191998; Pubmed-10725697;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIGAND BINDING, AND TISSUE SPECIFICITY. MEDLINE-20357357; PubMed-10781587;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunol. 164:3465-3470(2000).
                                                                                                                                                                                                                                                    InterPro; IPR003593; AAA_ATPase.
InterPro; IPR005129; ArgK.
                                                                                                                                                          EMBL; M91449; AAA23053.1; -.
EMBL; AAE00591; AAK24454.1; -.
PIR; B87557; B87557
PIR; S27534; S27534.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       264 ARAARRA 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ARAARRA 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GPR2 OR CCR10
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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Matches
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                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Utterback T., Weldman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-ATCC 19089 / CB15;
MEDLINE-21173698; PubMed-11259647;
MEDLINE-21173698; PubMed-11259647;
MACTIVE PROBLEM T.V., Laub M.T., Paulsen I.T., Nelson K.E., Elsen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R., Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B., DeBOY R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H., Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K., Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O. Salzberg S.L., Venter J.C., Shaplro L., Fraser C.M.;
"Complete genome sequence of Caulobacter crescentus.";
Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
                                                                                Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
Caulobacteraceae; Caulobacter.
NCBI_TaxID=155892;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-ATCC 19089 / CB15;
MEDLINE-93133840; PubMed-8421698;
Wang S.P., Sharma P.L., Schoenlein P.V., Ely B.;
"A histidine protein kinase is involved in polar organelle
                                                                                              laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE CBBY/CBBZ/GPH/YIEH FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36.8%; Score 7; DB 1; Length 291; 100.0%; Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR005834; Hydrolase.
Pfam; PF00702; Hydrolase; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 291 AA; 30694 MW; 750F090FB154E6E5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            development in Caulobacter crescentus.";
Proc. Natl. Acad. Sci. U.S.A. 90:630-634(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-ocr-1994 (Rel. 30, Created)
16-ocr-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Hypothetical protein CC2483.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   llarity 100.0%; Pred. No. 17; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                              EMBL; 270692; CAA94666.1; ALT_TERM.
EMBL; 270692; CAA94655.1; ALT_INIT.
EMBL; ACO7074; AAK46576.1; -.
TIGR; MT2292; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                          Tuberculist, Rv2232; -. Tuberculist, Rv2233; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caulobacter crescentus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
tes 7; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 RAAARRA 15
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P37895;
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Pred. No.

100.08;

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Best Local Similarity
Matches 7; Conserv
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A vierra M.A., Genovese M.C., Butcher E.C., Soler D.;
A novel Chemokine ilgand for CCR10 and CCR3 expressed by epithelial
Cells in mucosal tissues.;
J. Immunol. 165:2943-2949(2000).
TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIOM IONS
C. I. FUNCTION: RECEPTOR FOR CHEMOKINES SCYA27 AND SCYA28. SUBSEQUENTLY
C. I. FUNCTION: RECEPTOR FOR CHEMOKINES SCYA27 AND SCYA28. SUBSEQUENTLY
C. I. TISSUES PRECIPICATES CHEMOKINES IN A PRE-B CELL LINE.
C. I. TISSUE SPECIFICATY: EXPRESSED AT HIGH LEVELS IN ADULT TESTIS,
C. I. TISSUE SPECIFICATY: EXPRESSED AT HIGH LEVELS IN ADULT TESTIS,
C. I. TISSUE SPECIFICATY: EXPRESSED IN MAS
COBSERVED IN MANY OTHER ADULT TISSUES INCLUDING SPLEEN, THYMUS,
C. LYMPHOCYTES, THYROID AND SPINAL CORD. ALSO EXPRESSED BY
MELANOCYTES, THYROID AND SPINAL CORD. ALSO EXPRESSED EN
CELLS. ALSO DETECTED IN T CELLS AND IN SKIN-DERIVED LANGERHANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb.sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MIM: 600240; ...
MIM: 600240; ...
GO: GO:0005887; C:integral to plasma membrane; TAS.
GO: GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.
InterPro: IPR005382; CC_chemkinel0.
InterPro: IPR000276; GCC_Rhodpsn.
Pfam. PF00001; 7tm_1; 1.
Wang W., Soto H., Oldham E.R., Buchanan M.E., Homey B., Catron D., Jenkins N., Copeland N.G., Gilbert D.J., Nguyen N., Abrams J., Kershenovich D., Smith K., McClanahan T., Vicari A.P., Zlotnik A.; "Identification of a novel chemokine (CCL28), which binds CCR10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4
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2 (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
EXTRACELLUIAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
7 (POTENTIAL).
7 (POTENTIAL).
7 (POTENTIAL).
7 (POTENTIAL).
7 (POTENTIAL).
8 XIMIARITY.
BY SIMIARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; FROUZS; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein.
NOMAIN 1 52 EXTRACELULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     V -> L (IN REF. 3).
MISSING (IN REF. 2).
S -> C (IN REF. 2).
69DF12B639AEA99A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL).
                                                                                            Blol. Chem. 275:22313-22323(2000)
                                                                                                                                  LIGAND BINDING.
MEDLINE-20432268; Pubmed-10975800;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL: AF215981; AAF63709.1; -. EMBL: AF208237; AAF72871.1; -. EMBL: U13667; AAA64593.1; -. Genew; HGNC:4474; GPR2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR01557; CHEMOKINER10.
PRINTS; PR00237; GPCRRHODOPSN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               600240;
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DOMAIN
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CONFLICT
SEQUENCE
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                                                                             (GPR2)
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Length 362;

DB 1;

Score 7;

36.8%;

Query Match

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Prodom; PD004193; Argd; 1.
Prodom; PD004193; Argd; 1.
Argdine blosynthesis; Transferase; Acyltransferase.
Argdine blosynthesis; Transferase; Acyltransferase Alpha CHAIN
CHAIN 1 175 (BY SIMILARITY).
(BY SIMILARITY).

GLUTAMATE N-ACETYLTRANSFERASE BETA CHAIN
GLUTAMATE N-ACETYLTRANSFERASE BETA CHAIN
TOTAL OF TRANSFERASE BETA CHAIN
T
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CLEAVAGE (NONHYDROLYTIC) (BY SIMILARITY).
1605C5B17B7B05A8 CRC64;

    similarity).
    SUBCELIULAR LOCATION: Cytoplasmic (Probable).
    MISCELLANEOUS: Some Dacteria possess a monofunctional argJ, i.e., capable of catalyzing only the fifth step of the argJnine biosynthetic pathway.
    SIMILARITY: Belongs to the argJ family.

   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: N(2)-acetyl-L-ornithine + L-glutamate = L-ornithine + M-acetyl-L-glutamate.
-!- PATHWAX: Arginine Blosynthesis; fifth step.
-!- SUBDNIT: Reterotetramer of two alpha and two beta chains (By
                                                                                                                                                                                                                                                                                                                  15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Glutamate N-acetyltransferase (EC 2.3.1.35) (Ornithine acetyltransferase) (Ornithine transacetylase) (Ornithine Glutamate N-acetyltransferase) (Ontains: Glutamate N-acetyltransferase) (Ontains:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
   ö
   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sanchez R., Roovers M., Glansdorff N.; "Organisation of arginine biosynthetic genes in Thermus thermophilus.";
   ö
                                                                                                                                                                                                                                                                    381 AA.
   Mismatches
                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-98154436; PubMed-9493385;
   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                acetyltransferase beta chain].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40318 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HAMAP; MF_01106; -; 1.
InterPro; IPR002813; ArgJ.
Pfam; PF01960; ArgJ; 1.
Conservative
                                                                                                                                                                                                                                                                    STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thermus thermophilus
                                                                                         188.
381 AA;
                                                          3 AARRAAR 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thermus.
NCBI_TaxID-274;
                                                                                                                                                                                                                                                             ARGJ_THETH
P96137;
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365 AARRAAR 371

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                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                           Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Rabang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -1. CATALYTIC ACTIVITY: ATP + succinate + CoA - ADP + succinyl-CoA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              *Complete genome sequence of the model actinomycete Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           similarity).
-!- SIMILARITY: Belongs to the succinate/malate CoA ligase beta
subunit family.
                                      ö
                                                                                                                                                                                                                                 28-FEB-2003 (Rel. 41, Last sequence update)
15-SEB-2003 (Rel. 42, Last annotation update)
Succinyl-CoA synthetase beta chain 2 (EC 6.2.1.5) (SCS-beta 2).
SUCC OR SCO6585 OR SC8A6.06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- PATHWAY: Tricarboxylic acid cycle.
                                                                                                                                                                                                                                                                                                 Streptomyces coelicolor.
Sacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Streptomycineae, Streptomycetaceae, Streptomyces.
NCBL_raxID=1902;
      Length 381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 383;
                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00549; 11gase-cc., regrams; 1.
PIGRFAMS; TIGR01016; sucCoAbeta; 1.
PROSTTE; PS01217; SUCCINYL_COA_LIG_3; 1.
Ligase; Tricarboxylic acid cycle; Complete proteome.
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      DB 1;
                                                                                                                                                                                   383 AA.
                                   0; Mismatches
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100.0%; Pred. No. 22;
.tve 0; Mismatches
   36.8%; Score 7; I
                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro: IPR003135; ATP-grasp.
InterPro: IPR005809; CoA_lig_beta.
InterPro: IPR005811; CoA_ligase.
Pfam; PP03222; ATP-grasp; I.
Pfam; PP00549; Ilgase-CoA; I.
                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-A3(2) / M145;
MEDLINE-21996410; Pubmed-12000953;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AL939128; CAA19778.1; -. PIR; T35773. HSSP; P07460; 18CU. HANAP; MF.00558; -; 1.
                                                                                                                                                                                                                 28-FEB-2003 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100...
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              coelicolor A3(2).";
Nature 417:141-147(2002).
                                 7; Conservative
                                                                                                                                                                                   STANDARD;
                                                                                                  274 ARRAARA 280
                                                                   4 ARRAARA 10
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               phosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hopwood D.A.;
                                                                                                                                                                                   SIRCO
                                                                                                                                                 RESULT 8
SUC2_STRCO
                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                              Slesarev A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N., Shcherbinina O.V., Shakhova V.V., Balova G.I., Aravind L., Matale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O., Malykh A.G., Roonin E.V., Koryavkin S.A.; and Expense of hyperthermophile Methanopyrus kandleri Av19 and monophyly of archaeal methanogens."

Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).

- FUNCTION: Catalyzes two activities which are involved in the cyclic version of arginine biosynthesis: the synthesis of acetlyglutamate from glutamate and acetyl-COA, and of conithine by transacetylation between acetylornithine and glutamate (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROTEIN ARGJ ALPHA CHAIN (BY SIMILARITY).
ARGININE BLOSYNHESIS BIFUNCTIONAL
PROFEIN ARGJ BETA CHAIN (BY SIMILARITY).
ED311EC1F47DS6DD CR664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        similarity).
--- SUBCELLULAN LOCATION: Cytoplasmic (Probable).
--- MISCELLANEOUS: Some bacteria possess a monofunctional argJ, 1.e., capable of catalyzing only the fifth step of the arginine biosynthetic pathway.
--- SIMILARITY: Belongs to the argJ family.
                                                                                              15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Arginine biosynthesis bifunctional protein arg/ [includes: Glutamate N-acetyltransferase (EC 2.3.1.135) (Ornithine acetyltransferase)
(Ornithine transacetylase) (OATase); Amino-acid acetyltransferase (EC 2.3.1.1) (N-acetylglutamate synthase) (AGS)] (Contains: Arginine biosynthesis bifunctional protein arg/ alpha chain; Arginine biosynthesis bifunctional protein arg/ beta chain;
                                                                                                                                                                                                                                                                                               Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- CATALYTIC ACTIVITY: N(2)-acetyl-L-ornithine + L-glutamate = L-ornithine + N-acetyl-L-glutamate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -I- PATHWAY: Arginine blosynthesis; first step.
-I- PATHWAY: Arginine blosynthesis; fifth step.
-I- SUBGNIT: Heterotetramer of two alpha and two beta chains (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ARGININE BIOSYNTHESIS BIFUNCTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Probon; PD004193; ArgJ; 1.
TIGRFAMs; TIGR00120; ArgJ; 1.
Arginine blosynthesis; Multifunctional enzyme; Transferase;
Acyltransferase; Complete proteome.
                                    387 AA
                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-AV19 / DSM 6324 / JCM 9639;
MEDLINE-21927647; PubMed-11930014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE010376; AAM02078.1; -.
                                                                              (Rel. 42, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          387 AA; 41840 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HAMAP; MF_01106; atypical; 1. InterPro; IPR002813; ArgJ.
                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   387
                                                                                                                                                                                                                                                                          Methanopyrus kandleri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF01960; ArgJ
                                                                                                                                                                                                                                                                                                               Methanopyrus.
NCBI_TaxID=2320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  similarity)
                                                                                                                                                                                                                                                          ARGJ OR MKQB65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      glutamate.
                                                                         15-SEP-2003
                                  ARGJ_METKA
Q8TX15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SECTENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
                    ARGJ_METKA
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RESULT 9
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                                                    30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2013 (Rel. 41, Last annotation update)
38-MAY phosphate reductase (GPR) (EC 1.2.1.41) (Glutamate-5-
38-MAIdehyde dehydrogenase) (Glutamyl-gamma-semialdehyde
dehydrogenase) (GSA dehydrogenase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Euteleostom1;
                                                                                                                                                                                                                                             Melothermus ruber.
Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
Melothermus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wolecular cloning and sequence analysis of the proA gene from
                                                                                                                                                                                                                                                                                                                                                                                                                                            faklichkin S.Y., Zimina M.S., Yurchenko Y.V., Hromov I.S., Neumivakin L.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 417;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIGREAMS; TIGRO0407; pron; 1.
PROSITE; PS01223; PROA; 1.
Oxidoreductase; Proline blosynthesis; NADP.
SEQUENCE 417 AA; 44985 MW; A280ABA7E9C92268 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazos; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cat eye syndrome critical region protein 5 precursor CECR5.
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Last annotation update)
  417 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 7; DB 1; Pred, No. 23; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long modified and this statement is not removed entities requires a license spreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Interpro; IPR002086; Aldehyde_dehydr.
Interpro; IPR000965; Gglut_pp_reduct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09NX41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF082661; AAC72811.1; -.
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28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last seq
15-SEP-2003 (Rel. 42, Last sen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36.8%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00171; aldedh; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 AARAAAR 13
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                 MCBI_TaxID-277;
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PROA MEIRU
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SO THE SO THE SOURCE COUNTY SET SOURCE SOURC
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                                                                                                                                                                                                                                                                                                                                                                 15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Forkhead box protein D3 (HNF3/FH transcription factor genesis) (Winged hells protein CWH-3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Freyaldenhoven B.S., Freyaldenhoven M.P., Iacovonl J.S., Vogt "Aberrant cell growth induced by avian winged helix proteins. Cancer Res. 57:123-129(1997).
-I. FUNCTION: PROBABLE TRANSCRIPTION FACTOR.
-I. SUBCELLULAR LOCATION: Nuclear.
-I. SIMILARITY: Contains 1 fork-head domain.
                       Length 387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 394;
                                                                           0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JANAIN, SMOOJS); FORK, HEAD_1; 1.
PROSITE; PSO0657; FORK, HEAD_1; 1.
PROSITE; PSO0658; FORK, HEAD_2; 1.
PROSITE; PSS0039; FORK, HEAD_3; 1.
DNA-binding; Nuclear protein; Transcription regulation.
DONA-IN 67
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324A4B36B9E31899 CRC64;
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                    DB 1;
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100.0%; Pred. No. 22;
1ve 0; Mismatches
                                                                           Mismatches
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Pfam; PF00250; Fork_head; 1.
RINTS; PR00053; FORKHEAD.
PRODOM; PD0000425; TF_Fork_head; 1.
SWART; SW00339; FH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FISSUE=Embryo;
MEDLINE=97141794; PubMed=8988052;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U37274; AAC60066.1; -. HSSP; Q63245; 2HFH.
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Best Local Similarity 100.
           Query Match 36.8
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gallus gallus (Chicken).
                                                                                                                                                                                276 ARRAARA 282
                                                                                                                               4 ARRAARA 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 RAARRAA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T02495;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBL_TaxID-9031;
                                                                                                                                                                                                                                                                                                                     FXD3_CHICK
P79772;
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SEQUENCE
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Gaps

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RESULT 11 PROA_MEIRU

à 유 EMBL; AK001034; BAA91475.1; -. EMBL; AK000461; BAA91180.1; -. EMBL; BC042540; AAH42540.1; -.

AF273270; AK001034;

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P54138; 09CB50;
01-0CT-1996 (Rel. 34, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
28-FCB-2003 (Rel. 41, Last annotation update)
Bypothetical protein ML2443.
ML2443 OR U2168F OR B2168_C2_201.
                                                                                                                                                                                          Genew; HGNC:1843; CECR5.
Genew; HGNC:1843; CECR5.
InterPro; IPR006353; HAD_CECR5.
InterPro; IPR006357; HAD_SF_IIA.
TIGRRAMS; TIGR01456; CECR5; 1.
TIGRRAMS; TIGR01460; HAD-SF-IIA; 1.
Signal, Alternative splicing.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
Y486_MYCLE
ID Y486_MYCLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                    DORRADOR STATE TERMINATION SOLVER STATE TERMINATION SOLVER SOLVER
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Riausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B. Buetow R.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow R.H., Schaefer C.F., Bhat N.K.,
Bopkins R.F., Jordan H., More T., Max S.L., Wang J., Hasha F.,
A Bigleton M., Soarsa M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
A Brownstein M.J., Usdin T.B., Tochiyuki S., Carninci P., Frange C.,
A Brownstein M.J., Usdin T.B., Tochiyuki S., Carninci P., Frange C.,
A Basak S.A., McKernan N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McKernan B.J., Abramson R.D., Mullahy S.J.,
A Hillaton D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Cabbigues S., Sanchez A.,
A Whiting M., Madan A., Young A.C., Sheychenko Y., Bouffaug S., Sanchez A.,
Blakesley R.W., Touchman J.W., Green E.D., Dickeon M.C.,
Butterfield Y.S. N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S. N., Krzywinski M.I., Skalska U., Smailus D.E.,
And mounse Chun Schein J.E., Jones S.J.M., Marra M.A.;
And mounse Chun Schein J.E., Jones S.J.M., Marra M.A.;
And mounse Chun And Initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE SPECIFICITY: Widely expressed.

TISSUE SPECIFICITY: Widely expressed.

MISCELLANEOUS: Candidate gene for the Cat Eye Syndrome (CES), a developmental disorder associated with the duplication of a 2 Mb region of 22q1.2. Duplication usually takes in the form of a surpernumerary bisatellited isodicentric chromosome, resulting in four copies of the region (represents an inv dup(22)(q11)). CES is characterized clinically by the combination of coloboma of the fissues, preauricular tags and/or pits, frequent occurrence of heart and renal malformations, and normal or near-normal mental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM 2).

TISSEE—Embryo, and Gastric carcinoma;

Isogal T., Ota T., Hayashi K., Sudjama T., Otsuki T., Suzuki Y.,

Isogal T., Ota T., Bugano S., Shiratori A., Sudo H.,

Nishikawa T., Nagal K., Sugano S., Shiratori A., Sudo H.,

Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,

Takahashi M., Chiba T., Ishida S., Murakawa K., Ono Y., Takiguchi S.,

Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,

Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,

Ninomiya K., Iwayanagi T.;
SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
MEDLINE-21275466; Pubbed-11381032;
PCOLINE-21275466; Pubbed-11381032;
Bridgland L.J., Hu S., Birren B., Minoshima S., Shimizu N., Pan H.,
Nguyen T., Fang F., Fu Y., Ray L., Wu H., Shaull S., Phan S., Yao Z.,
Chen F., Huan A., Hu P., Wang Q., Loh P., Qi S., Roe B.A.,
                                                                                                                                                                                                                                                                                 "Analysis of the cat eye syndrome critical region in humans and the region of conserved synteny in mice: a search for candidate genes at or near the human chromosome 22 pericentromere.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "NEDO human cDNA sequencing project.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and mouse CDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Event_Alternative splicing; Named isoforms-2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                         Genome Res. 11:1053-1070(2001).
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Gaps

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Length 423; 0; Indels

DB 1; 24;

36.8%; Score 7;

423 AA; 46321 MW;

SEQUENCE

Pred. No. 24;

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100.08;

MAAWGCVAALGAARGLCWRAARAAAGLQGRPARRCYAVGPA POTENTIAL: CAT EYE SYNDROME CRITICAL REGION PROTEIN 5.

(in isoform 1)

-> MYAWFFLPSFS (1)/FIId=VSP_003840

41

VARSPLIC

CONFLICT

D -> N (IN REF. 2; BAA91180). V -> F (IN REF. 2; BAA91475). E -> G (IN REF. 2; BAA91475). C4D9208AB8B86CE CRC64;

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                                                                                                                                          Cole S.T., Eiglmeler K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Bonore N., Garnler T., Churcher C., Harris D., Mungall K., Basham D., Brown D., Chillingworth T., Connor R., Boarles R.M., Deviln K., Duthoy S., Feltwell T., Fraser A., Hamlin N., Holroyd S., Hornsby T., Jagels K., Lacrolx C., Maclean J., Moule S., Murphy L., Oliver K., Quall M.A., Rajandream M.A., Rutherford K.M., Rutherford K.M., Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
                                                                                                  MEDLINE-21128732; PubMed-11234002;
SEQUENCE FROM N.A.
```

Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.

Mycobacterium leprae.

428 AA

STANDARD;

Smith D.R., Robison K.; Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases

SEQUENCE FROM N.A.

NCBI_TaxID-1769

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development

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Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F., Alwes L.M.C., Ganarol L.B.A., Alwes L.M.C., Canarol L.B.A., Alwes L.M.C., Canarol L.B.A., Alves L.M.C., Canarol L.B.A., Alves L.M.C., Canarol L.B.A., Canarotte G., Canavan F., Cardozo J., Chambergo F., Ciaphna L.P., A Ciarla J.B. Ferreira A.J.S., Ferreira R.C.C., Ferrol M.I.T., Farla J.B., Ferreira R.D.S., Ferreira R.C.C., Ferrol M.I.T., A Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F., Locall E.C., Machado M.A., Madeira A.M.B.M., Martine F.G., Marchado M.A., Madeira A.M.B.M., Mayaki C.T., Moon D.H., Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R., Aphola L.A.F., Takita M.A., Tamura R.B., Teixeira E.C., Texting M.A., Tanidade dos Santos M., Truffil D., Tsai S.M., White F.F., Setubal J.C., Kiltajima J.P.;

Trindade dos Santos M., Truffil D., Tsai S.M., White F.F., Schubal J.C., Kiltajima J.P.;

Tomparison of the genomes of two Xanthomonas pathogens with differing what specificities and the setupance of two Xanthomonas pathogens with differing when the setupance of two Xanthomonas pathogens with differing when the setupance of two Xanthomonas pathogens with differing when the setupance of two Xanthomonas pathogens with differing when the setupance of two Xanthomonas pathogens with differing when the setupance of two Xanthomonas pathogens with differing the setupance of two Xanthom
                                                                                                                                                                                        Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.
NOBL_TaxID=92829;
                    28-FEB-2003 (Rel. 41, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) tRNA modification GTPase trmE. TRME OR THDF OR XAC4370.
                                                                                                                                                                Kanthomonas axonopodis (pv. citri)
                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-306 / ATCC 13902 / XV 101;
MEDLINE-22022145; Pubmed-12024217;
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                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE-94167875; PubMed-8122370;
Leung-Tack P., Audonnet J.F., Riviere M.;
The complete DNA sequence and the genetic organization of the short unique region (US) of the bovine herpesvirus type 1 (ST strain).";
Virology 199:409-421(1994).
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N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
0145942AA35B05CB CRC64;
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                                                                                                                                                                                                                                                                                                                   Length 428;
                                                                                                                                                                                                                                                                                                                                                                                0; Indels
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EMBL; U00018; AAA17228.1; ALT_INIT.
EMBL; AL583925; CAC31960.1; -.
PIR; H87214; H87214.
Leproma: ML2443; -.
InterPro; IPR001205; Glyco_trans_1.
Pfam; PF00534; Glycos_transf_1; 1.
Pypothetical protein; Complete proteome.
SEQUENCE 428 AA; 45291 MW; Al4F9F0187E3587C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bovine herpesvirus type 1.2 (strain ST).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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Pred. No. 25;
0; Mismatches
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1... 0; Mismatches
                                                                                                                                                                                                                                                                             Score 7; Db
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InterPro; IPR003363; Herpes_gG.
Pfam; PF02400; Herpes_gG; 1.
GJycoprotein; Transmembrane; Potent; SIGNAL
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                                                                                                                                                                                                                                                                                                                                       Local Similarity 100.
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ses 7; Conser
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Q08103;
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VGLX_HSVBS
AC 00810.3
DT 01-NOV
DT 0
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Nature 417:459-463(2002).

-!- FUNCTION: Exhibits a very high intrinsic GTPase hydrolysis rate.
-!- FUNCTION: Exhibits a very high intrinsic GTPase hydrolysis rate.
Involved in the blosynthesis of the hypermodified nucleoside 5-
methylaminomethyl-2-thiouridine, which is found in the wobble
position of some tRNAs (By similarity).
-!- SIMILARITY: Belongs to the era/trmE family of GTP-binding
proteins. TrmE subfamily.
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100.0%; Pred. No. 25;
tilve 0; Mismatches
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TRME_XANAC STANDARD;
AC 08PEH9;
DT 28-FEB-2003 (Rel. 41, Created)

RESULT 15